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(57) Abstract

This invention provides recombinant DNA molecules which code for polypeptides that exhibit the antigenicity of an *Aln g I* allergen of alder, *Alnus sp.*, of a *Cor a I* allergen of hazel or of a *Bet v I* allergen of birch and other plants of the order Fagales, and for polypeptides comprising at least one epitope thereof, as well as nucleic acids which under stringent conditions hybridize with such DNA sequences or are derivable from such sequences by degeneracy of the genetic code. In addition, methods are described for using the polypeptides coded by these DNA molecules and their use in the diagnosis or therapy of allergic diseases.

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ALLERGENS OF ALDER POLLEN AND APPLICATIONS THEREOF

1. FIELD OF THE INVENTION

The invention provides recombinant DNA molecules which code for polypeptides, and the polypeptides per se, that have at least one epitope of an Aln g I pollen allergen, or a Cor a I pollen allergen or a Bet v I pollen allergen of a tree of the order Fagales, particularly alder, Alnus sp., or the entire Aln g I allergen protein, particularly hazel, Corylus sp., or the entire Cor a I allergen protein, or particularly birch, Betula sp., or the entire Bet v I allergen protein, and exhibit the same or similar antigenicity as the Aln g I, the Cor a I or the Bet v I allergen. The invention also provides replicable microbial expression vehicles and microorganisms for use in processes for producing such allergenic polypeptides. Methods are provided for the diagnosis and therapy of allergic diseases using the synthetic polypeptides of the invention.

2. BACKGROUND OF THE INVENTION

It has long been known that a type I allergy to pollen proteins is associated with symptoms such as itchy and reddened eyes, running nose, swollen eyelids, coughing and asthmatic conditions. In this respect, the pollens of early-flowering trees of the order Fagales (e.g., birch, hazel, alder and hornbeam) hold an important position. Numerous studies have been carried out to identify and characterize the allergens of these pollens precisely (1 - 4). Progress with regard to the exact characterization of pollen allergens has been hindered by the heterogeneity of the pollen extracts currently in use. Some eight allergens of alder pollen elicit an IgE response in atopics and one of them, Aln g I, a 17 kD protein, reacts with a majority of the sera of allergic patients as the major allergen (5, 6).

At least 10 % of the population suffers from pollen allergies at various times and to varying extent. These allergies are mediated by IgE antibodies which react

with pollen proteins. The possibility exists for a therapy for pollen allergies by hyposensitization, i.e., by the regular and slowly increasing administration of the proteins producing the allergy.

Diagnostic methods for allergic diseases, such as radio-allergosorbent test (RAST), paper radioimmunosorbent test (PRIST), enzyme-linked immunosorbent assay (ELISA), radioimmunoassays (RIA), immuno-radiometric assays (IRMA), luminescence immunoassays (LIA), histamine release assays, and IgE immunoblots depend greatly upon the availability of pure allergens. Protein extracts from pollen isolated from natural sources are difficult to standardize because preparations vary from batch to batch. For example, they may contain unwanted constituents, and/or certain proteins may be lost in the extraction procedure and be missing from the final preparation (7). Clearly, diagnostic tests which employ well defined allergens that can be reproducibly prepared would be superior to tests which employ raw pollen extracts with an insufficiently defined mixture of allergens and other components. Recombinant DNA production of allergenic polypeptides, or allergenic fragments thereof, would allow more reproducible preparations of allergens of defined content for standardized diagnostic and therapeutic methods.

Allergens may be purified to homogenity from pollen by known protein/chemical methods, for example, by means of affinity chromatography (8). These methods are relatively costly and require pollen as an expensive source for allergens. It would, therefor, be cheaper and more efficient to use recombinant DNA methods to produce an allergenic protein, or fragments of that protein.

Hyposensitization has proved to be an effective therapy in allergic diseases. This therapy consists of parenteral or oral administration of allergens in increasing doses over a fairly long period of time.

3. SUMMARY OF THE INVENTION

The present invention provides recombinant DNA molecules which contain a nucleotide sequence that codes for a polypeptide which exhibits the same or similar antigenic properties as the major allergen, Aln g I, Cor a I or Bet v I of trees of the order Fagales, for example, of alder (Alnus sp.), hazel (Corylus sp.) or birch (Betula sp.) or a polypeptide which comprises at least one epitope of such allergens. The invention provides the complete cDNA sequence of an Aln g I, a Cor a I or a Bet v I allergen and hence the complete deduced amino acid sequences. Additionally, the invention includes (a) nucleotide sequences which hybridize with such a cDNA sequence under high stringency and encode a polypeptide having at least one epitope of an Aln g I, a Cor a I or a Bet v I allergen and (b) nucleotide sequences which can be derived from such allergenic polypeptides by degeneracy of the genetic code. This nucleotide sequence can be expressed as an Aln g I, a Cor a I or a Bet v I allergen, or as a polypeptide which comprises at least one epitope thereof. In a preferred embodiment, this cDNA sequence contains the whole sequence or parts of the sequence set forth in the Sequence Listing as SEQ ID NO. 2 for Aln g I, as SEQ.ID NO.10, 13, 16 and 19 for Cor a I and as SEQ ID NO. 22 for Bet v I.

As concerns their IgE binding, pollens of birch, alder, hazel and hornbeam possess similar major allergens which - so far as is known - exhibit a high degree of homology on the amino acid level. The present invention therefore relates not only to an Aln g I allergen of alder, or Cor a I of hazel or Bet v I of birch, but as well to Aln g I, Cor a I or Bet v I pollen allergens of other species which are coded by DNA allergen under stringent conditions or can be derived from such polypeptide allergens by degeneracy of the genetic code.

Hybridization of a polynucleotide with another polynucleotide under stringent conditions requires at least a 60 % identity between such polynucleotides at the nucleic acid level.

Such stringent conditions entail washing of hybridized nitrocellulose filters as follows:

(a) For DNA/DNA and DNA/RNA hybridizations: A temperature of 55°C, a salt concentration of 150 mM NaCl and 15 mM Na_3 citrate at pH 7,0, and a SDS (Sodium Dodecyl Sulfate) detergent at a concentration of 0,1 % (w/v).

(b) For oligodeoxynucleotide/DNA hybridizations: A temperature of 55°C, a salt concentration of 1M NaCl and 10 mM Na_3citrate x $2H_2O$ at pH 7,0, and a SDS (Sodium Dodecyl Sulfate) detergent at a concentration of 0,5 % (w/v). In this context "oligodeoxynucleotide" refers to an oligomer of a single-stranded DNA of up to 100 nucleotides in length.

In addition, this invention provides expression plasmids that contain a nucleotide sequence as described above and host cells which harbor these expression plasmids.

This invention also provides compositions containing synthetic polypeptides which exhibit the antigenicity of parts or of the whole of an alder Aln g I allergen or of allergens of other plants which, because of a high degree (at least 50 %) of amino acid homology (9), exhibit antigenic cross-reactivity to parts or to all of an alder Aln g I allergen, i.e., antibodies or cellular antigen binding sites which are actually directed to alder Aln g I allergen are likewise able to bind to these molecules. These synthetic polypeptides include fusion and nonfusion polypeptides which contain a polypeptide portion that possesses the antigenicity of a part or of all of an alder polypeptid which contain a polypeptide portion that possesses the antigenicity of a part or of all of an Aln g I, a Cor a I or a Bet v I allergen. The method for preparing such synthetic polypeptides comprises the steps of culturing of prokaryotic or eukaryotic host cells which contain an expression plasmid described above and purification of the synthetic polypeptide(s) from the culture.

The term "synthetic" here alternatively includes polypeptides which are prepared by cloning and expression of the nucleotide sequences described here or by chemical synthesis of polypeptides encoded by these nucleotide sequences.

The synthetic polypeptides which are produced according to this invention exhibit antigenicity the same as or similar to the native allergen. As shown below, a cDNA clone coding for an alder Aln g I, a hazel Cor a I or a birch Bet v I can be

used to produce a nonfusion polypeptide which reacts with IgE in the sera of allergic persons. It is therefore possible to use this polypeptide as an antigen in diagnostic tests (such as RAST, PRIST, ELISA, RIA, IRMA, LIA, histamine release assays and IgE immunoblots known in the art and referred to above), as a component of prophylactic or therapeutic agents in hyposensitization therapy, and as a component in any kind of in vivo diagnostic procedure such as bronchial, conjunctival, dermal, nasal and oral provocation and skin tests.

In particular, the synthetic allergens can be used as diagnostic reagents in vitro and in vivo, since their antigenicity corresponds to that of the native Aln g I pollen allergens and they are therefore able to bind IgE of sera of persons suffering from Aln g I pollen allergy. In the same way, the antigenicity corresponds to that of the native Cor a I or Bet v I pollen allergens and they are also able to bind IgE of sera of sensitive or allergic patients.

It is therefore one of the objects of the present invention to provide a method for the preparation of pollen allergens, in particular for Aln g I, Cor a I or Bet v I allergens, so as to have this family of allergens available for diagnostic tests for detection of the corresponding allergy and, alternatively, for hyposensitization therapy.

As main epitopes capable of modifying T-cell response the following amino acid sequences were found:

GlyValPheAsnTyrGlu

PheIleLeuAspGlyAspLysLeu

AlaIleSerSerValGluAsnIle

GlyAsnGlyGlyProGlyThrIleLysLysIleSerPhe

LysTyrValLysAspArgValAspGluValAsp

LeuLeuArgAlaValGluSerTyrLeuLeuAlaHisSer.

All these sequences are present in all said allergens, i.e. Aln g I, Cor a I and Bet v I.

4. BRIEF DESCRIPTION OF THE FIGURES

The following figures and description aid in understanding the field and scope of the invention.

FIG. 1 shows a cDNA (665 nucleotides, SEQ ID NO.1) encompassing the nucleotide sequence encoding an Aln g I allergen of alder. The cDNA sequence consists of a coding region of 483 nucleotides (including the initation and termination codons), a 3' noncoding region of 162 nucleotides and a poly-A tail of 20 nucleotides. The deduced amino acid sequence of alder Aln g I polypeptide is indicated in FIG. 1 under the respective codons. The complete protein has 160 (SEQ ID NO.3) amino acids (including the methionine of the initiation codon).

FIG. 2 shows the nucleotide sequence of the BP-A primer (SEQ ID NO.4) that was used for synthesis of the first cDNA strand. The recognition sequences of the restriction enzymes BglII (nucleotides 19-24) and HindIII (nucleotides 31-36) are underlined. The sequence of T7 primer (nucleotides 4-17), which was used as primer for the PCR amplification of Aln g I and is the constituent of BPA, is likewise indicated.

FIGS. 3 - 10 show Immunoblot analysis of isoforms of the major hazel pollen allergen Cor a I as recombinant non-fusion proteins, in particular

FIGS. 3 - 6:

An identical set of patients' sera was used to characterize the Cor a I isoforms (lanes 1 - 9).

Lanes B: buffer control without addition of patients' sera.

Lanes N: a pool of non-allergic normal human sera.

IgE antibodies from the allergic patients' sera, which bound to the isoforms, was detected by ^{125}I labeled rabbit-anti human IgE. Each of the isoforms shows reactivity with IgE from allergic patients' sera. All isoforms were able to bind IgE, although their individual binding pattern may differ from patient to patient.

FIG. 7:

An identical set of experiments was performed using E.coli JM 105 transformed with the plasmid pKK 223.3 without any cDNA insertion. No bound IgE could be detected.

FIG. 8:

Likewise the cDNA fragment whose sequence is shown in SEQ ID NO. 1 was ligated into the expression plasmid pKK 223.3. The protein corresponding to the coding region (see SEQ ID NO. 2 and SEQ ID NO.3) was expressed in E.coli JM 105 and tested with the identical set of patients' sera as above. rAln g I was able to bind IgE from these patients' sera in each case (lanes 1 - 9). In lanes B (buffer control, no patients' sera) and N (a pool of sera from non allergic individuals) no binding could be observed.

FIG. 9:

This represents the quality control of the patients' sera used in the above experiments. The very same set of sera was tested on separated and blotted proteins from an aqueous extract of birch pollen. IgE from every single serum bound strongly to the major allergen of birch pollen, Bet v I (lanes 1 - 9). No binding could be observed for the buffer control (lane B) and the pool of sera from non allergic individuals.

FIG.10:

Furthermore the same sera were tested on rBet v I and showed exactly the same strong reactivity with the recombinant nonfusion protein.

FIG. 11:

Inhibition experiment showing the capacity of rBet v I to bind IgE from tree pollen allergic patients' sera and thus to prevent the IgE from further binding to the corresponding hazel pollen allergen Cor a I. 1 ml each of a 1 : 10 dilution of birch pollen allergic individuals' sera (1 - 5), of a serum pool of non allergic individuals (6), and buffer without the addition of serum (7) was incubated over night at 4°C with the addition of 5 µg of rBet v I (panel 1), 5 µg of BSA (panel 2), or buffer only (panel 3). These samples were used to probe a Western blot of SDS-PAGE-separated

hazel pollen proteins. In the case where rBet v I had been added no IgE binding to the 17kD Cor a I could be observed. The addition of bovine serum albumin (BSA) or buffer without addition of a protein could not inhibit the binding of patients' IgE to the hazel Cor a I.

5. EXAMPLES

5.1. Poly A+ RNA isolation from pollen and synthesis of the first cDNA strand:

Polyadenylated (polyA+) mRNA was isolated from ripe alder pollen (Allergon AB, Engelsholm,Sweden) (l). Using this, the first strand of cDNA was synthesized as follows:

2 µl 10x buffer (480 mM Tris (hydroxymethyl) aminomethane (Tris), 60 mM $MgCl_2$, 400 mM KCl, pH 4,8)

2 µl 10 mM dithiothreitol (DTT)

1 µl primer BP-A (100 ng/µl, nucleotide sequence of FIG.2) (SEQ ID NO.4)

2 µl 25 mM deoxynucleoside triphosphates (dNTPs), i.e. 25 mM each of dATP, dCTP, dGTP, dTTP (Pharmacia, Uppsala, Sweden)

11 µl H_2O

1 µl poly A+RNA (3 µg)

1 µl AMV reverse transcriptase (United States Biochemical Corporation (USB), Cleveland, Ohio, USA) = 32 Units.

This reaction, with a total volume of 20 µl, was incubated for 2 hours at 42°C, then diluted 1 : 1 with 1x TE buffer (10 mM Tris, 1mM ethylenediamine tetraacetic acid (EDTA), pH 8,0) and stored at 4°C.

5.2 Polymerase chain reaction (PCR):

PCR was carried out on the hybrid RNA-DNA molecules prepared in Section 5.1. A mixture of the following two oligodeoxynucleotides was used as primer for the 5'-end of the molecules:

No. 2482 (SEQ ID NO.5)

5'- GTT TTC AAT TAC GAA GCG GAA AC -3'

No.2490 (SEQ ID NO.6)

5'- GTT TTC AAT TAC GAA GCG GAG AC -3'

The nucleotide sequences of these oligodeoxynucleotides were derived from the N-terminal amino acid sequence of alder Aln g I partially determined by Edman degradation and follwing the codon usage of birch (B. verrucosa).

T7 primer (SEQ ID NO.7) (Pharmmacia), which is likewise a constituent of the BP-A primer, was used as primer for the 3' end of the molecules. The following mixture was used for the reaction:

2,5 µl of the reaction mixture in Section 5.1

5,0 µl 10x PCR buffer (400 mM KCl, 10 mM $MgCl_2$, 10 % gelatin, 100 mM Tris, pH 8,3)

2,0 µl T7 primer (SEQ ID NO.7) (Pharmacia) = 20 pmol

4,0 µl primer mix in equal parts of No. 2482 (SEQ ID NO.5) and 2490 (SEQ ID NO.6) = 100 pmol

2,5 µl 2 mM dNTPs (Pharmacia)

1,5 µl 100 mM $MgCl_2$

32,5 µl H_2O (to 50 µl)

Addition of 1 unit Taq DNA polymerase (USB). The reaction mixture was incubated for 30 seconds at 93°C, for 30 seconds at 55°C and for 1 minute at 72°C. This cycle was run through 30x in all. Finally, the reaction mixture was kept at 72°C for another 10 minutes.

5.3 Cloning of the PCR fragment and sequencing:

The DNA fragment synthesized in Section 5.2 was isolated from a 1,5 % agarose gel by means of DEAE paper (10). This fragment was then kinased at the 5'-end.

a) Kinasing

10 µl DNA (= 500 ng Aln g I DNA)

2,5 µl 10x T4 polynucleotide kinase buffer (Boehringer, Mannheim, Germany)

7,0 µl γ-^{32}P-ATP, 10 mCi/ml (Amersham, Little Chalfont, England

4,5 µl H_2O

1,0 µl polynucleotide kinase (Boehringer)

The reaction mixture was incubated for 20 minutes at 37°C. After that another addition of 1 µl polynucleotide kinase was made and the mixture was incubated for 60 minutes at 37°C.

b) Klenow fill-in reaction:

To the above reaction mixture was added:

1 µl 2mM dNTPS (Pharmacia)

1 µl Klenow Fragment (= 2 units)

The kinased and filled-in DNA fragment was purified by way of a Nick™ Column (Pharmacia) and was then precipitated with ethanol and sodium acetate (9).

c) BglII digestion of fragment:

Several restriction enzyme sites were added at the 3'-end to the Aln g I sequence through the use of the BP-A oligodeoxynucleotide (FIG.2; SEQ ID NO.4) in the PCR. The BglII site in this sequence was selected for cleavage with the restriction enzyme, BglII, to ligate the fragment in the corresponding BglII site of pBluescript^R plasmid (Stratagene, LaJolla, California, USA). Due to the Klenow reaction, blut ends had already been produced at the 5'-end of the sequence. All the DNA precipitated in Section 5.3b was dissolved in 2 µl 10x BglII buffer (Boehringer). 17 µl H_2O and 1 µl BglII (11 units) were added. The reaction mixture was incubated for 1,5 hours at 37°C. The fragment so cut was eluted from a 1,5% agarose gel by means of DEAE paper (10).

d) Ligation of the DNA fragment in pBluescript^R KS+ plasmid:

pBluescript^R KS+ plasmid (Stratagene) was selected as cloning vector and cut with the restriction enzymes EcoRV (supplies flush ends; the 5'-end of the Aln g I fragment is ligated to these) and BamHI (supplies staggered ends compatible with BglII; the 3'-end of the Aln g I fragment is ligated to these). The phosphate groups at the 5'-ends of the plasmid were removed by alkaline phosphatase (12) to prevent non-specific religation of the vector.

Ligation of Aln g I fragment in pBluescript^R KS+ plasmid:

20 ng DNA from Section 5.3c dissolved in 10 µl H_2O

2,0 µl 10x ligation buffer (200 mM Tris, 50 mM $MgCl_2$, 50 mM DTT, 500 µg/ml bovine serum albumin; pH 7,6)

1,0 µl 10 mM ATP

3,0 µl pBluescript^R KS+ cut with EcoRV and BamHI (= 50 ng)

4,0 µl H_2O

1,0 µl T4 DNA ligase Boehringer (= 3 units)

This reaction was incubated for 4 hours at room temperature.

e) Transformation of competent E.coli host cells:

Transformation was carried out in E.coli XL1-Blue cells (Stratagene) (13). The selection of positive clones was carried out on ampicillin-containing (100 µg/ml) culture plates by means of the blue-white indication system (14).

f) Sequencing of Aln g I DNA:

Sequencing of Aln g I DNA was carried out by means of a T7 sequencing kit (Pharmacia), according to the manufacturer's instructions.

5.4 Expression of Aln g I DNA and detection of IgE binding of the resulting proteins:

a) The DNA insert from the pBluescript^R KS+ vector, which contains the coding sequence for Aln g I, was subjected to mutagenesis according to Kunkel et al (15). To complete the Aln g I sequence at the 5'-end and provide it with the ATG codon and an additional EcoRI site, the following oligodeoxynucleotide was synthesized (SEQ ID NO.8): 5'-CTT CGT AAT TGA AAA CAC CCA TGA ATT CCG ATA CCG TCG A -3' and used for mutagenesis. This enabled the Aln g I sequence to be ligated, in the correct orientation, by means of the EcoRI site at the 5'-end and by means of the HindIII site at the 3'-end of the gene in the expression plasmid pKK 223-3 (Pharmacia). E.coli Kl2 JMl05 cells (thi, rpsL, endA, sbcBl5, hsdR4, delta (lacpro AB)/F', thraD36, proAB, lacI^{q}Z delta Ml5) were transformed with this plasmid. After protein synthesis was effected, the bacterial cells were harvested and bro-

ken up with liquid nitrogen. The lysate was separated n a SDS polyacrylamide gel. Detection of recombinant Aln g I nonfusion protein was done by means of immunoblot. IgE in the sera of allergic patients was bound by the recombinant Aln g I. Detection of bound IgE was effected by ^{125}I-labeled antihuman IgE (Pharmacia).

b) The DNA insert in pBluescript^{R} KS+ plasmid, which contains the sequence coding for Aln g I, was ligated by means of EcoRI linkers (Boehringer) in the expression plasmids pEX A, pEX B and pEX C (16), which shift the reading frame of the insert one nucleotide each time. In this way, in one case the correct reading frame for Aln g I was obtained and the production of a recombinant Aln g I fusion protein was induced. The capability of this recombinant Aln g I fusion protein to bind IgE in sera of patients allergic to alder pollen was shown by means of immunoblot. Detection of bound IgE was effected by ^{125}I-labeled antihuman IgE (Pharmacia).

An analogous method was applied for the cloning and expressing of Cor a I.

5.5 Expression of Cor a I DNA and detection of IgE binding of the resulting protein

The cDNA fragments whose sequences are shown in SEQ ID NO.9, 12, 15 and 18 were ligated into the expression plasmid pKK 223.3 (Pharmacia LKB Biotechnology, Uppsala, Sweden). The proteins corresponding to the coding region (see SEQ ID NO.10, 13, 16 and 19) of these fragments were expressed in E.coli JM 105 transformed with the respective recombinant plasmids. Cultures were grown until the OD_{600} reached 0,4. Isopropyl-β-D-galactopyranoside was then added to a final concentration of 0,5 mM and the cultures grown at 37°C over 3,5 hours for expression of recombinant non-fusion proteins. Bacterial cells were harvested by centrifugation, taken up in 50 mM Tris-HCl buffer, pH 7,5, containing 220 mM NaCl and the cells were disrupted by a freezethaw cycle. The supernatant containing the recombinant non-fusion proteins was loaded onto a 15 % SDS-PAGE. The separated proteins were transferred to a nitrocellulose filter. IgE-binding proteins were detected by the use of allergic patients' sera.

The results are shown in FIGS. 3 - 6.

5.6 Test of reaction of T-cell epitopes

Peripheral blood was collected from birch pollen allergic patients who showed igE reactivity to Bet v I exclusively, as demonstrated by Western Blot. Peripheral mononuclear cells (PBMC; the white blood cell fraction containing the lymphocytes) were isolated by density gradient centrifucation. Allergen specific T-cells were enriched by culturing PBMC in presence of Bet v I. After a cloning procedure, T-cell clones (TCC) were proved to react with the complete Bet v I molecule by a proliferation assay, showing that in presence of the specific allergen a proliferation occurs, which is at least 10-fold higher than the autoproliferative activity of the TCC, as measured by ^{3}H-Thymidine incorporation. Two Bet v I specific TCC isolated from atopic donors reacted in the same way with the above mentioned peptides as with the whole Bet v I molecule, proving that these peptides represent or contain the relevant T-cell epitopes.

TCC	TCC+FC	TCC+FC+Bet v I	TCC+FC+PEPTIDE	
443	960	30516	31580*	cpm
160	508	21218	23309**	cpm

FC: feeder cells

cpm: counts per minute

* peptide: LLRAVESYLLAHS

**peptide: KYVKDRVDEVD

6. METHODS OF ADMINISTRATION

The present invention covers the use of the recombinant or synthetic polypeptide allergens to treat a mammal using such polypeptides alone or in combination with any pharmaceutically acceptable carriers or diluents, in accordance with standard pharmaceutical practice.

The method of treatment involves the administration of such a polypeptide allergen or parts thereof by any route of administration, that is bronchial, conjunctival, dermal, enteral, nasal, oral or vaginal. A range of from 1 picogram to 10 milligrams per application can be used. The diluents and carriers can be chosen by those skilled in the art according to commonly accepted galenic procedures. Like diagnostic methods, it requires pure and well defined allergens. The use of purified recombinant allergens or synthetic peptides would greatly reduce the risk of sensitizing patients to unwanted components.

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SEQUENCE LISTING

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(iii) NUMBER OF SEQUENCES: 23

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(B) COMPUTER: IBM PC compatible
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(D) SOFTWARE: WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 07/683,831
(B) FILING DATE: 11-APR-91
(C) CLASSIFICATION:

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(B) REGISTRATION NUMBER: 20,280
(C) REFERENCE/DOCKET NUMBER: 6530-009

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 665 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA of mRNA
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: No
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Alder (Alnus sp.)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGGGTGTTT TCAATTACGA AGCGGAAACC CCCTCCGTTA TCCCAGCGGC TCGGCTGTTC 60
AAGGCCTTTA TCCTTGATGG CGATAAGCTC CTTCCAAAGG TTGCACCTGA AGCTGTTAGC 120
AGTGTTGAGA ACATTGAAGG AAATGGAGGG CCTGGAACCA TCAAGAAGAT CACCTTTCCC 180
GAAGGCAGCC CTTTTAAGTA CGTAAAGGAG AGGGTTGATG AGGTTGATCG CGTAAACTTC 240
AAATACAGCT TCAGCGTGAT CGAGGGTGGT GCCGTGGGCG ACGCACTGGA GAAGGTCTGT 300
AACGAGATCA AGATAGTGGC AGCCCCTGAT GGAGGATCCA TCTTGAAGAT CAGCAACAAG 360
TTCCACACCA AAGGCGACCA TGAGATAAAT GCAGAGCAGA TTAAGATTGA AAAAGAAAAG 420
GCCGTGGGAC TTCTCAAGGC CGTTGAGAGC TACCTCTTGG CACACTCTGA TGCCTACAAC 480
TAAATTCTGC CTAATTTTGA TCAGCTTGCA TGTGTTCTTG TCAAGCCATA AATACTGCTT 540
AACTTCGTCT TGCTAATAAA TGAAGCTGTT GTAGTCGTTT ATGAGTACGT AATAATGACA 600
CCAAACATAT GGAGCCAATT GCTTATGAAT AGAAGTTAAG TTCTTAAAAA AAAAAAAAAA 660
AAAAA 665

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA of mRNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Alder (Alnus sp.)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGGTGTTT TCAATTACGA AGCGGAAACC CCCTCCGTTA TCCCAGCGGC TCGGCTGTTC 60
AAGGCCTTTA TCCTTGATGG CGATAAGCTC CTTCCAAAGG TTGCACCTGA AGCTGTTAGC 120
AGTGTTGAGA ACATTGAAGG AAATGGAGGG CCTGGAACCA TCAAGAAGAT CACCTTTCCC 180
GAAGGCAGCC CTTTTAAGTA CGTAAAGGAG AGGGTTGATG AGGTTGATCG CGTAAACTTC 240
AAATACAGCT TCAGCGTGAT CGAGGGTGGT GCCGTGGGCG ACGCACTGGA GAAGGTCTGT 300
AACGAGATCA AGATAGTGGC AGCCCCTGAT GGAGGATCCA TCTTGAAGAT CAGCAACAAG 360
TTCCACACCA AAGGCGACCA TGAGATAAAT GCAGAGCAGA TTAAGATTGA AAAAGAAAAG 420
GCCGTGGGAC TTCTCAAGGC CGTTGAGAGC TACCTCTTGG CACACTCTGA TGCCTACAAC 480

(4) INFORMATION FOR SEQ ID NO:3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: polypeptide
(iii) HYPOTHETICAL: No
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Alder (Alnus sp.)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Gly Val Phe Asn Tyr Glu Ala Glu Thr Pro Ser Val Ile Pro Ala
1 5 10 15

AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu Leu Pro
20 25 30

Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Glu Gly Asn
35 40 45

Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gly Ser Pro
50 55 60

Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Val Asn Phe
65 70 75 80

Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly Asp Ala Leu
85 90 95

Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro Asp Gly Gly
100 105 110

Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly Asp His Glu
115 120 125

Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val Gly Leu
130 135 140

Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Ala Tyr Asn
145

(5) INFORMATION FOR SEQ ID N : 4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other nucleic acid-synthetic
(iii) HYPOTHETICAL: Yes
(ix) FEATURE:
(D) OTHER INFORMATION: Primer for reverse transcription
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTTAATACGA CTCACTATAG ATCTCCCGGG AAGCTTTTTT TTTTTTTTTT 50

(6) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other nucleic acid-synthetic
(iii) HYPOTHETICAL: Yes
(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL/ISOLATE: 2482
(ix) FEATURE:
(D) OTHER INFORMATION: Primer for polymerase chain reaction (PCR) utilized at the 5' end of Aln g I mRNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
GTTTTCAATT ACGAAGCGGA AAC 23

(7) INFORMATION FOR SEQ ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other nucleic acid-synthetic
(iii) HYPOTHETICAL: Yes
(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: 2490
(ix) FEATURE:
(D) OTHER INFORMATION: Primer for polymerase chain reaction utilized at the 5' end of Aln g I mRNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
GTTTTCAATT ACGAAGCGGA GAC 23

(8) INFORMATION FOR SEQ ID NO: 7:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other nucleic acid-synthetic
(iii) HYPOTHETICAL: Yes
(ix) FEATURE:
(D) OTHER INFORMATION: Primer for polymerase chain reaction (PCR) utilized at the 3' end of Aln g I mRNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
AATACGACTC ACTA 14

(9) INFORMATION FOR SEQ ID NO: 8:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other nucleic acid-synthetic
(iii) HYPOTHETICAL: Yes
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
CTTCGTAATT GAAAACACCC ATGAATTCCG ATACCGTCGA 40

INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 619 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA of mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: hazel (*Corylus sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 9

```
ATGGGTGTTT TCAATTACGA GGTTGAGACT CCCTCCGTTA TCCCTGCGGC      50
AAGGCTGTTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG     100
TTGCACCTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG     150
CCTGGAACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA     200
CGTGAAGGAG AGGGTTGATG AGGTTGACAA CACAAACTTC ACATACAGCT     250
ACACCGTGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAGGTCTGC     300
CACGAGCTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT     350
CAGCAGCAAG TTCCACGCCA AAGGCGACCA TGAGATTAAT GCAGAGGAGA     400
TGAAGGGTGC CAAAGAAATG GCAGAGAAAC TTTTAAGGGC GGTTGAGACC     450
TACCTATTGG CACACTCTGC TGAATACAAC TAAATATCGT CTTGTGTCTT     500
CGCCCAATAA TAACTTGTAC GTGGCTTTCA TGTTTTTTTT AAAAAACTTT     550
GTTTACTTGC TAATAAAGGA GCTTGCGGTT GTGTTCATCT GCTTGCTGAA     600
AAAAAAAAAA AAAAAAAAA                                      619
```

INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA of mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: hazel (*Corylus sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 10

ATGGGTGTTT TCAATTACGA GGTTGAGACT CCCTCCGTTA TCCCTGCGGC 50
AAGGCTGTTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG 100
TTGCACCTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG 150
CCTGGAACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA 200
CGTGAAGGAG AGGGTTGATG AGGTTGACAA CACAAACTTC ACATACAGCT 250
ACACCGTGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAGGTCTGC 300
CACGAGCTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT 350
CAGCAGCAAG TTCCACGCCA AAGGCGACCA TGAGATTAAT GCAGAGGAGA 400
TGAAGGGTGC CAAAGAAATG GCAGAGAAAC TTTTAAGGGC GGTTGAGACC 450
TACCTATTGG CACACTCTGC TGAATACAAC 480

INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS: Cor a I 5 (c)
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear
(ii) MOLECULE TYPE: polypeptide
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: not applicable
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: hazel (*Corylus sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 11

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Met	Gly	Val	Phe	Asn	Tyr	Glu	Val	Glu	Thr	Pro	Ser	Val	Ile	Pro

16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
Ala	Ala	Arg	Leu	Phe	Lys	Ser	Tyr	Val	Leu	Asp	Gly	Asp	Lys	Leu

31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
Ile	Pro	Lys	Val	Ala	Pro	Gln	Ala	Ile	Thr	Ser	Val	Glu	Asn	Val

46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Glu	Gly	Asn	Gly	Gly	Pro	Gly	Thr	Ile	Lys	Asn	Ile	Thr	Phe	Gly

61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
Glu	Gly	Ser	Arg	Tyr	Lys	Tyr	Val	Lys	Glu	Arg	Val	Asp	Glu	Val

76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
Asp	Asn	Thr	Asn	Phe	Thr	Tyr	Ser	Tyr	Thr	Val	Ile	Glu	Gly	Asp

91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
Val	Leu	Gly	Asp	Lys	Leu	Glu	Lys	Val	Cys	His	Glu	Leu	Lys	Il

106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
Val	Ala	Ala	Pro	Gly	Gly	Gly	Ser	Ile	Leu	Lys	Ile	Ser	Ser	Lys

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121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
Phe His Ala Lys Gly Asp His Glu Ile Asn Ala Glu Glu Met Lys

136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
Gly Ala Lys Glu Met Ala Glu Lys Leu Leu Arg Ala Val Glu Thr

151 152 153 154 155 156 157 158 159 160
Tyr Leu Leu Ala His Ser Ala Glu Tyr Asn
```

INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 742 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA of mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: hazel (*Corylus sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 12

```
ATGGGTGTTT TCAATTACGA GGTTGAGACT CCCTCCGTTA TCCCAGCGGC      50
AAGGCTGTTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG     100
TTGCACCTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG     150
CCTGGAACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA     200
CGTGAAGGAG AGGGTTGATG AGGTTGACAA CACAAACTTC AAATATAGCT     250
ACACCGTGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAGGTCTGC     300
AGCGAGCTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT     350
CAGCAGCAAG TTCCACGCCA AAGGCGACCA TGAGATTAAT GCAGAGGAGA     400
TGAAGGGTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC     450
TACCTATTGG CACACTCTGC TGAATACAAC TAAATATCGT CTTGTGTCTT     500
CGCCCAATAA TAACTTGTAC GTGGCTTTCA TGTTTTTTTT TTAAAACTTT     550
GATTACTTGC TAATAAAGGA GCTTGCGGTT GTGTTCATCT GCTTGCTGAA     600
ATCGATGTTG TAACTCGGAA GAATGCAAAC TGAATGTTGT ATTACTTTTT     650
GCATATATAC AAATAATGGA AAGGATAACA TCATTGAAGT TCAAAAAAAA     700
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA            742
```

INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA of mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: hazel (*Corylus sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 13

```
ATGGGTGTTT TCAATTACGA GGTTGAGACT CCCTCCGTTA TCCCAGCGGC     50
AAGGCTGTTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG    100
TTGCACCTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG    150
CCTGGAACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA    200
CGTGAAGGAG AGGGTTGATG AGGTTGACAA CACAAACTTC AAATATAGCT    250
ACACCGTGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAGGTCTGC    300
AGCGAGCTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT    350
CAGCAGCAAG TTCCACGCCA AAGGCGACCA TGAGATTAAT GCAGAGGAGA    400
TGAAGGGTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC    450
TACCTATTGG CACACTCTGC TGAATACAAC                          480
```

INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear
(ii) MOLECULE TYPE: polypeptide
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: not applicable
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: hazel (*Corylus sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 14

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Met	Gly	Val	Phe	Asn	Tyr	Glu	Val	Glu	Thr	Pro	Ser	Val	Ile	Pro

16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
Ala	Ala	Arg	Leu	Phe	Lys	Ser	Tyr	Val	Leu	Asp	Gly	Asp	Lys	Leu

31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
Ile	Pro	Lys	Val	Ala	Pro	Gln	Ala	Ile	Thr	Ser	Val	Glu	Asn	Val

46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Glu	Gly	Asn	Gly	Gly	Pro	Gly	Thr	Ile	Lys	Asn	Ile	Thr	Phe	Gly

61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
Glu	Gly	Ser	Arg	Tyr	Lys	Tyr	Val	Lys	Glu	Arg	Val	Asp	Glu	Val

76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
Asp	Asn	Thr	Asn	Phe	Lys	Tyr	Ser	Tyr	Thr	Val	Ile	Glu	Gly	Asp

91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
Val	Leu	Gly	Asp	Lys	Leu	Glu	Lys	Val	Cys	Ser	Glu	Leu	Lys	Ile

106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
Val	Ala	Ala	Pro	Gly	Gly	Gly	Ser	Il	Leu	Lys	Ile	S r	Ser	Lys

```
121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
Phe His Ala Lys Gly Asp His Glu Ile Asn Ala Glu Glu Met Lys

136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
Gly Ala Lys Glu Met Ala Glu Lys Leu Leu Arg Ala Val Glu Thr

151 152 153 154 155 156 157 158 159 160
Tyr Leu Leu Ala His Ser Ala Glu Tyr Asn
```

INFORMATION FOR SEQ ID NO: 15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 655 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA of mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: hazel (*Corylus sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 15

ATGGGTGTTT TCAATTACGA GGCTGAGACC ACCTCCGTTA TCCCTGCGGC 50
AAGGCTGTTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG 100
TTGCACCTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG 150
CCTGGAACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA 200
CGTGAAGGAG AGGGTTGATG AGGTTGACAA CACAAACTTC ACATACAGCT 250
ACACCGTGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAGGTCTGC 300
CACGAGCTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT 350
CAGCAGCAAG TTCCACGCCA AAGGTGACCA TGAGATTAAT GCAGAGGAGA 400
TGAAGGGTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC 450
TACCTATTGG CACACTCTGC TGAATACAAC TAAACCTCGT CTTGTGTCTT 500
CGCCCAATAA TAGCTTGTAC GTGGCTTTCA TGTTTTTTTT TTAAACTTTG 550
TTTTCTTGCT AATAAAGGAG CTTGCGGTTG TGTTCATCTG CTTGCTGAAG 600
ATCGATGTTG TAACTCGGAA GAATGCAAAT TTAATGTTGT ATTAAAAAAA 650
AAAAA 655

INFORMATION FOR SEQ ID NO: 16

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA of mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) FRAGMENT TYPE: not applicable

(vi) ORIGINAL SOURCE:

(A) ORGANISM: hazel (*Corylus sp.*)

(vii) IMMEDIATE SOURCE:

(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN

(viii) POSITION IN GENOME: not applicable

(ix) FEATURE: not applicable

(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 16

```
ATGGGTGTTT TCAATTACGA GGCTGAGACC ACCTCCGTTA TCCCTGCGGC     50
AAGGCTGTTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG    100
TTGCACCTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG    150
CCTGGAACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA    200
CGTGAAGGAG AGGGTTGATG AGGTTGACAA CACAAACTTC ACATACAGCT    250
ACACCGTGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAGGTCTGC    300
CACGAGCTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT    350
CAGCAGCAAG TTCCACGCCA AAGGTGACCA TGAGATTAAT GCAGAGGAGA    400
TGAAGGGTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC    450
TACCTATTGG CACACTCTGC TGAATACAAC                          480
```

INFORMATION FOR SEQ ID NO: 17

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: not applicable

(v) FRAGMENT TYPE: not applicable

(vi) ORIGINAL SOURCE:

(A) ORGANISM: hazel (*Corylus sp.*)

(vii) IMMEDIATE SOURCE:

(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN

(viii) POSITION IN GENOME: not applicable

(ix) FEATURE: not applicable

(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 17

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Met	Gly	Val	Phe	Asn	Tyr	Glu	Ala	Glu	Thr	Thr	Ser	Val	Ile	Pro

16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
Ala	Ala	Arg	Leu	Phe	Lys	Ser	Tyr	Val	Leu	Asp	Gly	Asp	Lys	Leu

31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
Ile	Pro	Lys	Val	Ala	Pro	Gln	Ala	Ile	Thr	Ser	Val	Glu	Asn	Val

46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Glu	Gly	Asn	Gly	Gly	Pro	Gly	Thr	Ile	Lys	Asn	Ile	Thr	Phe	Gly

61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
Glu	Gly	Ser	Arg	Tyr	Lys	Tyr	Val	Lys	Glu	Arg	Val	Asp	Glu	Val

76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
Asp	Asn	Thr	Asn	Phe	Thr	Tyr	Ser	Tyr	Thr	Val	Ile	Glu	Gly	Asp

91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
Val	Leu	Gly	Asp	Lys	Leu	Glu	Lys	Val	Cys	His	Glu	Leu	Lys	Ile

106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
Val	Ala	Ala	Pr	Gly	Gly	Gly	Ser	Ile	Leu	Lys	Ile	S r	Ser	Lys

121	122	123	124	125	126	127	128	129	130	131	132	133	134	135

```
Phe His Ala Lys Gly Asp His Glu Ile Asn Ala Glu Glu Met Lys

136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
Gly Ala Lys Glu Met Ala Glu Lys Leu Leu Arg Ala Val Glu Thr

151 152 153 154 155 156 157 158 159 160
Tyr Leu Leu Ala His Ser Ala Glu Tyr Asn
```

INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 860 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA of mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: hazel (*Corylus sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 18

ATGGGTGTTT TCAATTACGA GGTTGAGACC CCCTCCGTTA TCTCAGCGGC 50
AAGGCTGTTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG 100
TTGCACCTCA AGCTATTACC AGCGTTGAAA ACGTTGGAGG AAATGGAGGG 150
CCTGGAACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA 200
CGTGAAGGAG AGGGTTGATG AGGTTGACAA CACAAACTTC AAATATAGCT 250
ACACCGTGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAAGTCTGC 300
AGCGAGCTGA AGATAGTGGC AGCCCCTGGT GGGGGATCCA CCTTGAAGAT 350
CAGCAGCAAG TTCCACGCCA AAGGTGACCA TGAGATTAAT GCAGAGGAGA 400
TGAAGGGTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC 450
TACCTATTGG CACACTCTGC TGAATACAAC TAAATATCGT CTTGTGTCTT 500
CGCCAATAAT AACTTGTACG TGGCTTTCAT GTTTTTTTTT AAAAAACTTT 550
GTTTACTTGC TAATAAAGGA GCTTGCGGTT GTGTTCATCT GCTTGCTGAA 600
ATCGATGTTG TAACTCGGAA GAATGCAAAC TGAATGTTGT ATTACTTTTT 650
GCATATATAC AAATAATGGA AAGGATAACA TCATTGAAGT TCAAAAAAAA 700
GAAAAAAAAA AGCTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTGTCA 750
ATTTTAACCC GATACTGATA CTCAAAAATG CAAGAGAGTT TCCGCATAAG 800
CACAATTTGT TTATGTTGAC TTAATACATT ATAAGCAAAA AAAAAAAAAA 850
AAAAAAAAAA 860

INFORMATI N FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA of mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: hazel (*Corylus sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 19

```
ATGGGTGTTT TCAATTACGA GGTTGAGACC CCCTCCGTTA TCTCAGCGGC     50
AAGGCTGTTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG    100
TTGCACCTCA AGCTATTACC AGCGTTGAAA ACGTTGGAGG AAATGGAGGG    150
CCTGGAACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA    200
CGTGAAGGAG AGGGTTGATG AGGTTGACAA CACAAACTTC AAATATAGCT    250
ACACCGTGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAAGTCTGC    300
AGCGAGCTGA AGATAGTGGC AGCCCCTGGT GGGGGATCCA CCTTGAAGAT    350
CAGCAGCAAG TTCCACGCCA AAGGTGACCA TGAGATTAAT GCAGAGGAGA    400
TGAAGGGTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC    450
TACCTATTGG CACACTCTGC TGAATACAAC                          480
```

INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear
(ii) MOLECULE TYPE: polypeptide
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: not applicable
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: hazel (*Corylus sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 20

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Met	Gly	Val	Phe	Asn	Tyr	Glu	Val	Glu	Thr	Pro	Ser	Val	Ile	Ser

16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
Ala	Ala	Arg	Leu	Phe	Lys	Ser	Tyr	Val	Leu	Asp	Gly	Asp	Lys	Leu

31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
Ile	Pro	Lys	Val	Ala	Pro	Gln	Ala	Ile	Thr	Ser	Val	Glu	Asn	Val

46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Gly	Gly	Asn	Gly	Gly	Pro	Gly	Thr	Ile	Lys	Asn	Ile	Thr	Phe	Gly

61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
Glu	Gly	Ser	Arg	Tyr	Lys	Tyr	Val	Lys	Glu	Arg	Val	Asp	Glu	Val

76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
Asp	Asn	Thr	Asn	Phe	Lys	Tyr	Ser	Tyr	Thr	Val	Ile	Glu	Gly	Asp

91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
Val	Leu	Gly	Asp	Lys	Leu	Glu	Lys	Val	Cys	Ser	Glu	Leu	Lys	Ile

106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
Val	Ala	Ala	Pro	Gly	Gly	Gly	Ser	Thr	Leu	Lys	Ile	Ser	Ser	Lys

```
121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
Phe His Ala Lys Gly Asp His Glu Ile Asn Ala Glu Glu Met Lys

136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
Gly Ala Lys Glu Met Ala Glu Lys Leu Leu Arg Ala Val Glu Thr

151 152 153 154 155 156 157 158 159 160
Tyr Leu Leu Ala His Ser Ala Glu Tyr Asn
```

INFORMATION FOR SEQ ID NO: 21

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 672 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA of mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) FRAGMENT TYPE: not applicable
(vi) ORIGINAL SOURCE:
(A) ORGANISM: birch (*Betula sp.*)
(vii) IMMEDIATE SOURCE:
(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
(viii) POSITION IN GENOME: not applicable
(ix) FEATURE: not applicable
(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 21

```
ATGGGTGTTT TCAATTACGA AACTGAGACC ACCTCTGTTA TCCCAGCAGC      50
TCGACTGTTC AAGGCCTTTA TCCTTGATGG CGATAATCTC TTTCCAAAGG     100
TTGCACCCCA AGCCATTAGC AGTGTTGAAA ACATTGAAGG AAATGGAGGG     150
CCTGGAACCA TTAAGAAGAT CAGCTTTCCC GAAGGCTTCC CTTTCAAGTA     200
CGTGAAGGAC AGAGTTGATG AGGTGGACCA CACAAACTTC AAATACAATT     250
ACAGCGTGAT CGAGGGCGGT CCCATAGGCG ACACATTGGA GAAGATCTCC     300
AACGAGATAA AGATAGTGGC AACCCCTGAT GGAGGATCCA TCTTGAAGAT     350
CAGCAACAAG TACCACACCA AAGGTGACCA TGAGGTGAAG GCAGAGCAGG     400
TTAAGGCAAG TAAAGAAATG GGCGAGACAC TTTTGAGGGC CGTTGAGAGC     450
TACCTCTTGG CACACTCCGA TGCCTACAAC TAATTAATTA ACTTGTGTCG     500
TCTCGAACAT GTCCCTGATC AATAATGGGT TGCAGTGTTC ATGGTGTTTT     550
TTGGGTCTAA TAAAGGAGCT TGCAGTTGTG ATCATCTGCT TGCTAGCTGA     600
AGATGTTGTA ATTTATTGGG AGAATGATAA TAAATGTTCT ATTAAAAAAA     650
AAAAAAAAAA AAAAAAAAAA AA                                   672
```

INFORMATION FOR SEQ ID NO: 22

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA of mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) FRAGMENT TYPE: not applicable

(vi) ORIGINAL SOURCE:

(A) ORGANISM: birch (*Betula sp.*)

(vii) IMMEDIATE SOURCE:

(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN

(viii) POSITION IN GENOME: not applicable

(ix) FEATURE: not applicable

(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 22

```
ATGGGTGTTT TCAATTACGA AACTGAGACC ACCTCTGTTA TCCCAGCAGC     50
TCGACTGTTC AAGGCCTTTA TCCTTGATGG CGATAATCTC TTTCCAAAGG    100
TTGCACCCCA AGCCATTAGC AGTGTTGAAA ACATTGAAGG AAATGGAGGG    150
CCTGGAACCA TTAAGAAGAT CAGCTTTCCC GAAGGCTTCC CTTTCAAGTA    200
CGTGAAGGAC AGAGTTGATG AGGTGGACCA CACAAACTTC AAATACAATT    250
ACAGCGTGAT CGAGGGCGGT CCCATAGGCG ACACATTGGA GAAGATCTCC    300
AACGAGATAA AGATAGTGGC AACCCCTGAT GGAGGATCCA TCTTGAAGAT    350
CAGCAACAAG TACCACACCA AAGGTGACCA TGAGGTGAAG GCAGAGCAGG    400
TTAAGGCAAG TAAAGAAATG GGCGAGACAC TTTTGAGGGC CGTTGAGAGC    450
TACCTCTTGG CACACTCCGA TGCCTACAAC                          480
```

INFORMATION FOR SEQ ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: not applicable

(v) FRAGMENT TYPE: not applicable

(vi) ORIGINAL SOURCE:

(A) ORGANISM: birch (*Betula sp.*)

(vii) IMMEDIATE SOURCE:

(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN

(viii) POSITION IN GENOME: not applicable

(ix) FEATURE: not applicable

(x) PUBLICATION INFORMATION: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 23

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Met	Gly	Val	Phe	Asn	Tyr	Glu	Thr	Glu	Thr	Thr	Ser	Val	Ile	Pro

16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
Ala	Ala	Arg	Leu	Phe	Lys	Ala	Phe	Ile	Leu	Asp	Gly	Asp	Asn	Leu

31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
Phe	Pro	Lys	Val	Ala	Pro	Gln	Ala	Ile	Ser	Ser	Val	Glu	Asn	Ile

46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Glu	Gly	Asn	Gly	Gly	Pro	Gly	Thr	Ile	Lys	Lys	Ile	Ser	Phe	Pro

61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
Glu	Gly	Phe	Pro	Phe	Lys	Tyr	Val	Lys	Asp	Arg	Val	Asp	Glu	Val

76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
Asp	His	Thr	Asn	Phe	Lys	Tyr	Asn	Tyr	Ser	Val	Ile	Glu	Gly	Gly

91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
Pro	Ile	Gly	Asp	Thr	Leu	Glu	Lys	Ile	Ser	Asn	Glu	Ile	Lys	Ile

106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
Val	Ala	Thr	Pro	Asp	Gly	Gly	Ser	Ile	Leu	Lys	Ile	S r	Asn	Lys

121	122	123	124	125	126	127	128	129	130	131	132	133	134	135

Tyr His Thr Lys Gly Asp His Glu Val Lys Ala Glu Gln Val Lys

136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
Ala Ser Lys Glu Met Gly Glu Thr Leu Leu Arg Ala Val Glu Ser

151 152 153 154 155 156 157 158 159 160
Tyr Leu Leu Ala His Ser Asp Ala Tyr Asn

CLAIMS

1. A recombinant DNA molecule, comprising a DNA coding for a polypeptide having at least one epitope of an allergen of trees of the order Fagales, the allergen is selected from the group Aln g I, Cor a I or Bet v I.

2. A recombinant DNA molecule according to claim 1, wherein the allergen Aln g I, Cor a I or Bet v I is selected from the group consisting of birch, alder, hazel and hornbeam.

3. A recombinant DNA molecule according to claim 1, wherein the epitopes of the allergens having an amino acid sequence selected from the following group

GlyValPheAsnTyrGlu

PheIleLeuAspGlyAspLysLeu

AlaIleSerSerValGluAsnIle

GlyAsnGlyGlyProGlyThrIleLysLysIleSerPhe

LysTyrValLysAspArgValAspGluValAsp

LeuLeuArgAlaValGluSerTyrLeuLeuAlaHisSer

4. A recombinant DNA molecule according to claim 1 having at least 60% identity to the nucleotid sequence as shown in SEQ ID No. 2.

5. A recombinant DNA molecule according to claim 1, wherein the allergen is an Aln g I allergen of alder.

6. A recombinant DNA molecule according to claim 1, 2, 3, 4 or 5 which codes for a polypeptide having the entire amino acid sequence of an Aln g I allergen.

7. A recombinant DNA molecule according to claim 5, which codes for a polypeptide having all or part of the amino acid sequence as defined in the Sequence Listing by SEQ ID NO:3.

8. A recombinant DNA molecule according to claim 1, wherein the allergen is a Cor a I allergen of hazel.

9. A recombinant DNA molecule according to claim 1 or 8, which codes for a polypeptide having the entire amino acid sequence of a Cor a I allergen.

10. A recombinant DNA molecule according to claim 1 having at least 60% identity to the nucleotid sequence as shown in SEQ ID NOs. 10, 13, 16, and 19.

11. A recombinant DNA molecule according to claim 8 which codes for a polypeptide having all or part of the amino acid sequence as defined in the Sequence Listing by SEQ ID NOs. 11, 14, 17, and 20.

12. A recombinant DNA molecule according to claim 1 wherein the allergen is a Bet v I allergen of birch.

13. A recombinant DNA molecule according to claim 1 having at least 60% identity to the nucleotid sequence as shown in SEQ ID No. 22.

14. A recombinant DNA molecule according to claim 12, which codes for a polypeptide having all or part of the amino acid sequence as defined in the Sequence Listing by SEQ ID NO. 23.

15. A recombinant DNA molecule according to claim 3 which codes for one of the epitopes of the allergens as listed in claim 3.

16. A polypeptide having at least one epitope of an Aln g I, a Cor a I or a Bet v I allergen showing the same or a similar capacity to bind IgE from tree pollen allergic individual's sera.

17. A replicable prokaryotic or eukaryotic expression vehicle capable, in a transformant prokaryotic or eukaryotic host organism, of being replicated and of directing expression of a DNA of claim 1 to 15 to produce said polypeptides.

18. A prokaryotic or eukaryotic host organism transformed with an expression vehicle capable, in said host organism, of being replicated and of directing expression of a DNA of claim 1 to 15 to produce said polypeptides.

19. A host organism according to claim 18, wherein the organism is Escherichia coli.

20. A method for producing a polypeptide having at least one epitope of an Aln g I, a Cor a I or a Bet v I allergen, comprising culturing a prokaryotic or eukaryotic host organism containing an expression vehicle capable, in said host organism, of being replicated and of directing expression of a DNA of claim 1 to 15 to produce said polypeptides.

21. A composition comprising a polypeptide having at least one epitope of an Aln g I, a Cor a I or a Bet v I allergen and produced by a method according to claim 20.

22. A composition comprising a polypeptide having at least one epitope of an Aln g I allergen and produced by a chemical synthesis according to amino acid sequence as defined in the Sequence Listing by SEQ ID NO. 3.

23. A composition comprising a polypeptide having at least one epitope of a Cor a I allergen and produced by a chemical synthesis according to amino acid sequence as defined in the Sequence Listing SEQ ID NOs.11, 14, 17 and 20.

24. A composition comprising a polypeptide having at least one epitope of a Bet v I allergen and produced by chemical synthesis according to the amino acid sequence as defined in the Sequence Listing by SEQ ID No. 23.

25. An isolated allergenic peptide of pollen of trees of the order Fagales, having at least one of the epitopes with amino acid sequence listed in claim 3.

26. A peptide according to claim 6, 7, 8, 9, 11, 12, 14, or 25, capable of modifying in a sensitive individual to whom it is administered, an allergic response to a pollen of a tree of the order Fagales.

27. A peptide according to claim 26 capable of modifying T-cell response to a pollen of trees of the order Fagales.

28. An isolated peptide of the claim 6, 7, 8, 9, 11, 12, 14 or 25 capable of interfering with an allergic response.

29. A method for detecting IgE antibodies comprising contacting serum of a mammal with a composition according to claim 21, and detecting any immunological reaction between IgE antibodies in the serum and said polypeptide having at least one epitope of an Aln g I, a Cor a I or a Bet v I allergen.

30. A method for detecting allergic reactions to an Aln g I, a Cor a I or a Bet v I allergen, comprising challenging a mammal with a composition according to claim 21 so as to elicit bronchial, conjunctival, dermal, nasal or oral provocation of said

mammal, and detecting any immunological reaction between said tissues and said polypeptides.

31. A method for detecting in vitro a cellular reaction to an Aln g I, a Cor a I or a Bet v I allergen , comprising contacting mammalian cells with a composition according to claim 21, and detecting any reaction between said cells and said polypeptide.

32. A method for treating a mammal afflicted with a pollen allergy, comprising administering an effective amount of a composition according to claim 21 to hyposensitize said mammal to an Aln g I, a Cor a I or a Bet v I allergen.

Aln g I

```
 1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20
ATG GGT GTT TTC AAT TAC GAA GCG GAA ACC CCC TCC GTT ATC CCA GCG GCT CGG CTG TTC
Met Gly Val Phe Asn Tyr Glu Ala Glu Thr Pro Ser Val Ile Pro Ala Ala Arg Leu Phe

21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38  39  40
AAG GCC TTT ATC CTT GAT GGC GAT AAG CTC CTT CCA AAG GTT GCA CCT GAA GCT GTT AGC
Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu Leu Pro Lys Val Ala Pro Glu Ala Val Ser

41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58  59  60
AGT GTT GAG AAC ATT GAA GGA AAT GGA GGG CCT GGA ACC ATC AAG AAG ATC ACC TTT CCC
Ser Val Glu Asn Ile Glu Gly Asn Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro

61  62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80
GAA GGC AGC CCT TTT AAG TAC GTA AAG GAG AGG GTT GAT GAG GTT GAT CGC GTA AAC TTC
Glu Gly Ser Pro Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Val Asn Phe

81  82  83  84  85  86  87  88  89  90  91  92  93  94  95  96  97  98  99 100
AAA TAC AGC TTC AGC GTG ATC GAG GGT GGT GCC GTG GGC GAC GCA CTG GAG AAG GTC TGT
Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly Asp Ala Leu Glu Lys Val Cys

101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
AAC GAG ATC AAG ATA GTG GCA GCC CCT GAT GGA GGA TCC ATC TTG AAG ATC AGC AAC AAG
Asn Glu Ile Lys Ile Val Ala Ala Pro Asp Gly Gly Ser Ile Leu Lys Ile Ser Asn Lys

121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140
TTC CAC ACC AAA GGC GAC CAT GAG ATA AAT GCA GAG CAG ATT AAG ATT GAA AAA GAA AAG
Phe His Thr Lys Gly Asp His Glu Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys

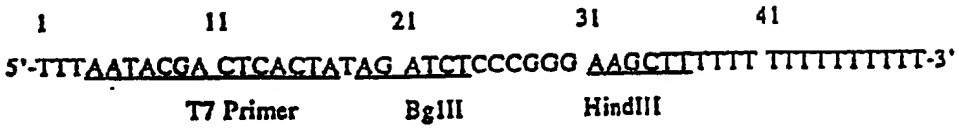
141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160
GCC GTG GGA CTT CTC AAG GCC GTT GAG AGC TAC CTC TTG GCA CAC TCT GAT GCC TAC AAC
Ala Val Gly Leu Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Ala Tyr Asn

161
TAA ATTCTGCCTAATTTTGATCAGCTTGCATGTGTTCTTGTCAAGCCATAAATACTGCTTAACTTCGTCTTGCTAATA
End

AATGAAGCTGTTGTAGTCGTTTATGAGTACGTAATAATGACACCAAACATATGGAGCCAATTGCTTATGAATAGAAGTT
AAGTTCTTAAAAAAAAAAAAAAAAAAAA
```

Figur 1

FIGURE 2


1
11
21
31
41
5'-TTTAATACGA CTCACTATAG ATCTCCCGGG AAGCTTTTTT TTTTTTTTTT-3'
T7 Primer
BglII
HindIII

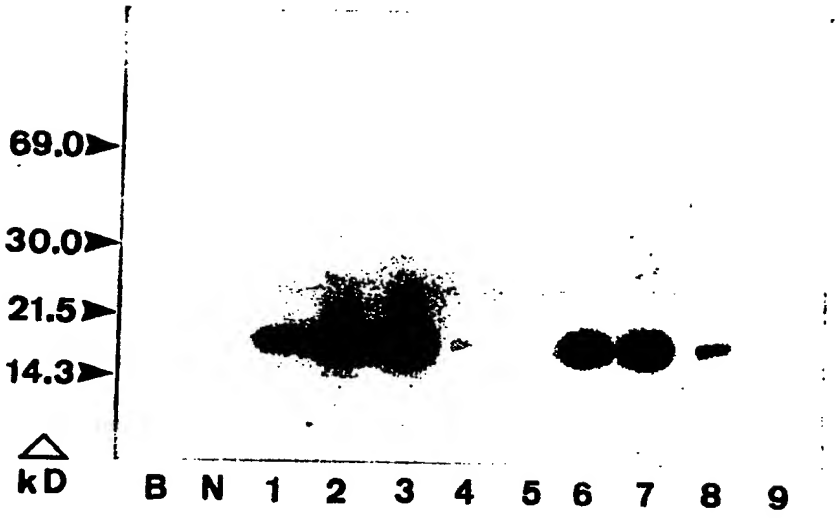

69.0
30.0
21.5
14.3
kD
B N 1 2 3 4 5 6 7 8 9

FIG. 3

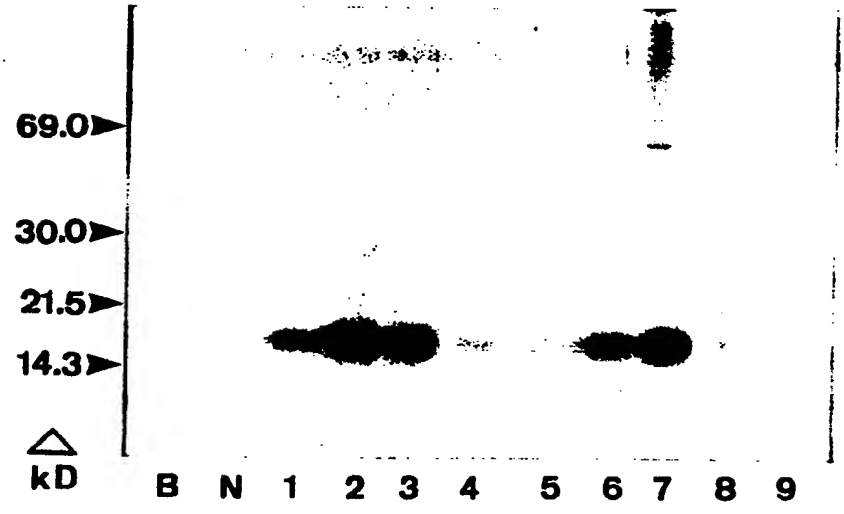
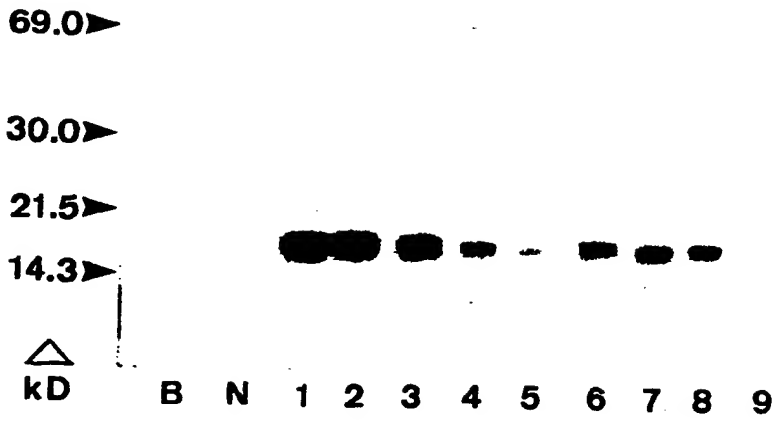

69.0
30.0
21.5
14.3
kD
B N 1 2 3 4 5 6 7 8 9

FIG. 4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30.0
21.5
14.3
kD
B N 1 2 3 4 5 6 7 8 9

Fig. 5

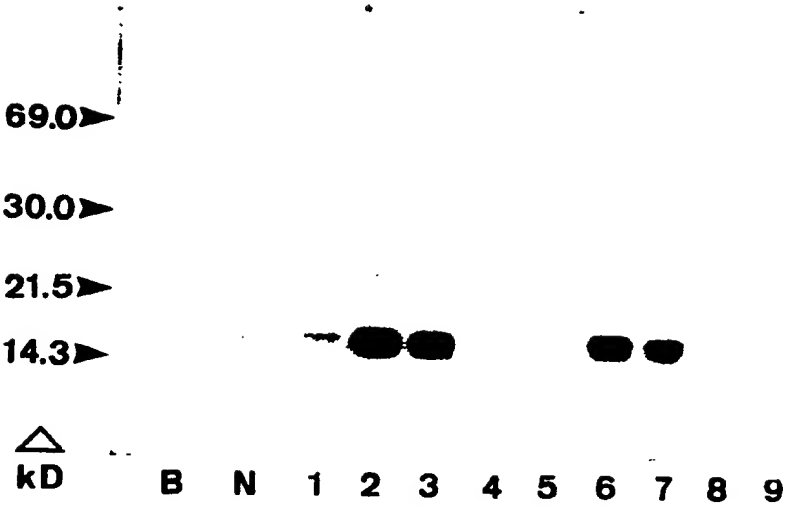
69.0
30.0
21.5
14.3
kD
B N 1 2 3 4 5 6 7 8 9

Fig. 6

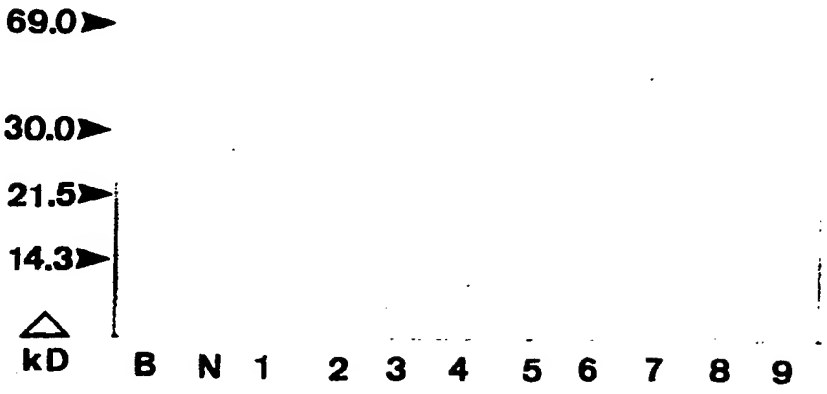
69.0
30.0
21.5
14.3
kD
B N 1 2 3 4 5 6 7 8 9

FIG. 7

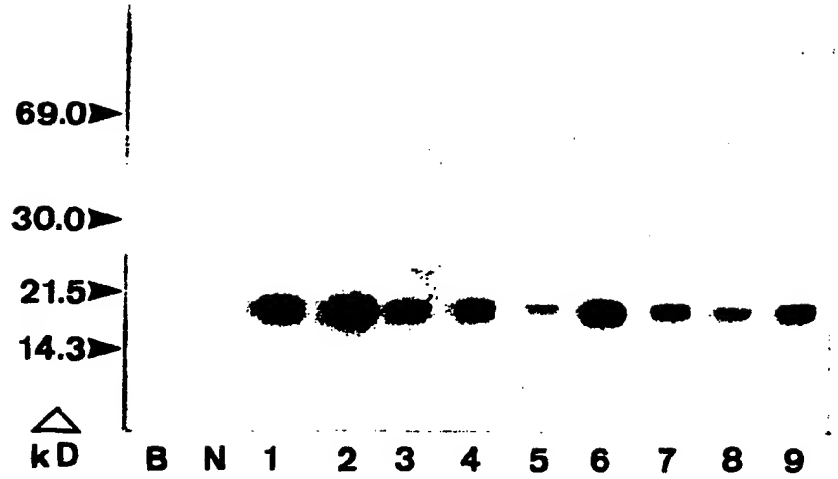
69.0
30.0
21.5
14.3
kD
B N 1 2 3 4 5 6 7 8 9

FIG. 8

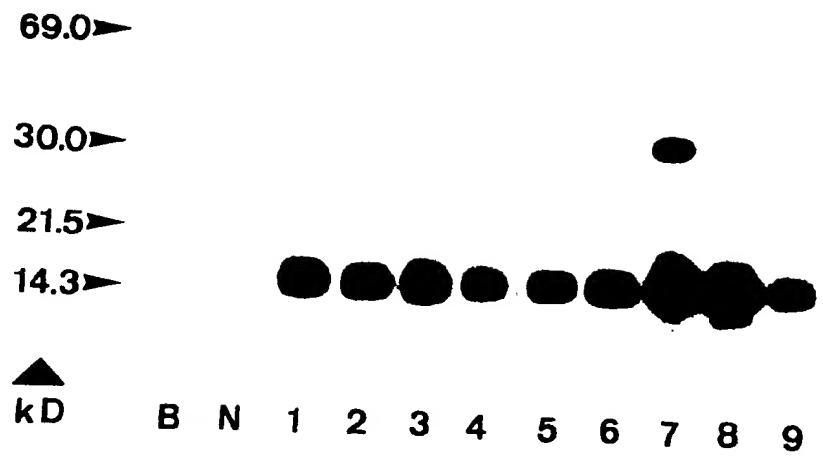
69.0
30.0
21.5
14.3
kD
B N 1 2 3 4 5 6 7 8 9

FIG. 9

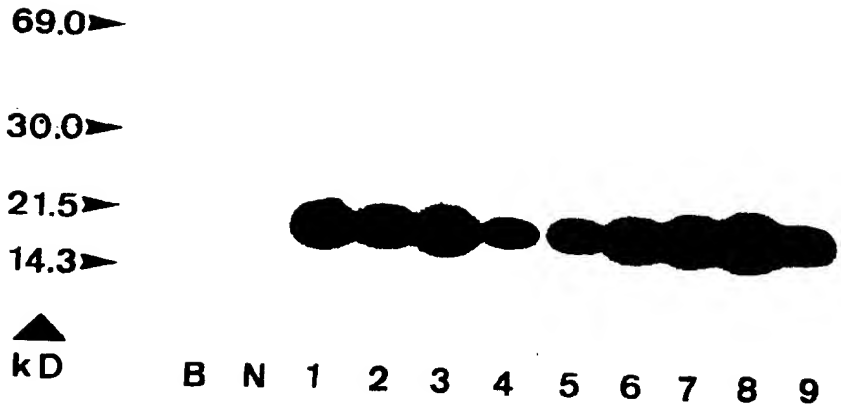
69.0
30.0
21.5
14.3
kD
B N 1 2 3 4 5 6 7 8 9

FIG. 10

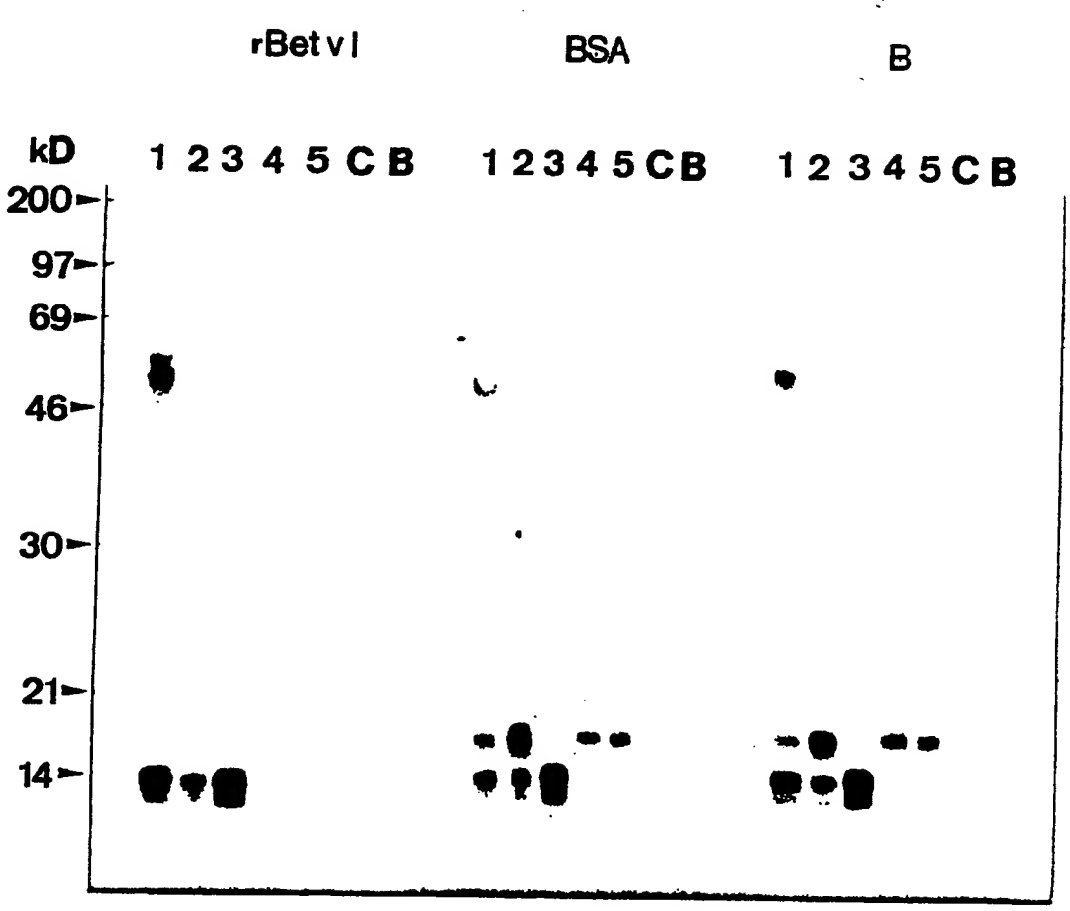

FIG. 11